## SEQUENCE LISTING:

## **SEQ ID NO:1** Amino acid sequence of mGy12.

- 5 1 MSSKTASTNS IAQARRTVQQ LRLEASIERI KVSKASADLM SYCEEHARSD
  - 51 PLLMGIPTSE NPFKDKKTQI IL\*

## SEQ ID NO:2 cDNA sequence of mGγ12, variant 1

10 CTAGAATTCA GCGGCCGCTG AATTCTAGGC GACGACGGCG AAGAGTGAGT 1 GCCAAGGTTC ATATGGGAAG GACTTTGGGG TGAGCATCTT CTCTATTTCC 51 101 AGCTGGCTTT TCTGATTTTC AGAAAGAAGA CTCATCAAAG ATGTCCAGCA AGACGGCAAG CACCAACAGC ATAGCCCAAG CCAGGAGAAC TGTGCAGCAG 151 15 CTGAGATTGG AAGCCTCCAT CGAAAGAATA AAGGTCTCAA AAGCATCAGC 201 251 AGACCTGATG TCATACTGTG AGGAGCATGC CCGGAGCGAC CCCCTGCTGA TGGGCATACC GACCTCAGAA AACCCGTTCA AGGATAAGAA GACCTGCATC 301 351 ATCTTATAGT GGACCAGGAA GCGCCCCTTG CCTCTTAACG CAAACCACAG CAGCAACCTG AAGGGATTCC TTCAGCTTAC CTGGTAACCA CAGCTAGTAA 401 CTAAAACACC CTTCTCTCGG AATAATAGAC CCTGAAGTCT CTCTTTTTCA 451 501 AGTTGTCCTT TCTTCACCCT TTACTGATTT AATACAGAAT AACAATCTTA 551 TTTTCTATTT GATAACTATG GTATCATATT GGGTTACTGT ATAAGGAAAA 601 TGGCAGGGGA GTTGTGGGAA GCTTGTCTTT ACAAAATATA ATTGATTAAG 651 ATATGTCAAG ACCTACATTG TCTAAGCACQ GGCAAATTAA AATGTCGAGA 25 701 ATCACTTCAG TCAAAAACCT TTATATTCTG\TTCTTAATAA TGTTTGTGCC 751 AACCTATATC CCATGTAAGG GATCTGGGGA GGAGGCATGT GTCTACAACC ATACCTTTTT GCACTATGGG CACTAACCAC CCTGAAACTT CCTGCGGTAG 801 CTCCCTCCCT TCAGAGTTAC ATCATTATCC TQACTCTGTG TAGGTAAATT 851 901 TCCGTGAAAT TTTTGTACAA AAAAAAGGTA ATGAAAGAAC GTTGCAAAGA 30 951 TCATCTGCAT TATAATGAGT TGATGCTGTT CTCACTCCTC TCTTGGAATT 1001 GTGCTGGCCC CTTAGTCTAC AATAAACTGT GCCAATTAAA AACCTAAGGC 1051 TAAAACTGAA AGCCCTTTGA TGGGGTCTTA ACTCATATCA GTCATTTGGG 1101 CTTCTCTGAT CCTGAGGCTA AGAAAGGGGA AGAGAQCCTC AGGAGGCAGC TTCCACTCCA GGGCTCTTGA TCTCTGCTGG ATTGGGGGTG GCCACCTCAG 1151

1351 CTTACTGCTA GAGCAGCTGC TTGTAGAGGG ACATTCCCTC CTTCCCAGTT 5 1401 TTAACTGGTG GACCACAGTG GGGGGAAAAA CATTCAAGCG ATATAAAGAC ACTTGGGCTC TTTGCAGATG CCTATACTTC CAACACTACC ATGTCCACAA 1451 1501 ACCACCCTGG GGGAGGGCCC TTCCAAAGGG AGGCTTGCTA GTTTCAGCGT CTAGCAGTTG GGTCCTCACT TTTACTCCAA TTGTGAAAAT AGCCCACGTA 1551 1601 CCCTCGCAGT GTCCAGTAGG GATCCCAGAG GCACATAACC AAGAAAGGAT 10 1651 TTTGACTTTG TOACAGTGAC TATTTAAAAT AATCTATTCG AAGTCCAAAC 1701 CAAACACAAA GCCTGTGATA TTTTAGGTTA TTAAGGTAAC TGCTAATGAA GGATTTTAAA AAGT&TCCTC AAAAAGGACT TAGCCCCGGG AGTTGTTTAT 1751 13 ١J AAAATTTCCC CCACTTGTAT ACAGTGTGCA CTAAAAGAAA ATGTATTTTA 1801 ĮĢ ATATCTAATG CCTGGGGTCT GAGCGTCATG CTTCTTGGTG GTAAACATGC ij 1851 15 1901 AGTCCTGTTC CTAAGTGACT CAGAGGCATC AGAATTTCTC CACGTTACCC ATCTGCTTGG CACTCGGAAC TGAGCGTGTG AAATCCATAG CGCTGCCCAC 1951 2001 AACCTGTTCT CACTGCTTAG CTCCCAGCTG GATTAAAGAC ACCTGCTCAG 4..... 4...4 4..... 4...4 2051 GCGGGAGAGA GAGAGAGAGA GCGAGCTTTT ACCTTGGAAA AGGTAAAGAT And the state of GGAAATGTAC ACCAAAAAAG AQAATTTTTA CATTTAATGG AACATTCTTT 2101 TTTTTTACAA GTATATTTTT CTACTGATAG TTTCAGAACA CTAATCTTAT 20 2151 2201 ATTCACTCTA ATCTTAAACA TGTTVCTTTA AATATTTATA AGGCAGTTTA 2251 TTACAGAATA TTTTCATGCA ATCAT&TGCA CATTATTGGT AGCAAACATA 2301 GTATATCCTT TAGTACTTTA GCATATTTTT GTTAAAATAC TTTTAATGGT 2351 AAGAAATGAA CTTGAGGTCC CAGGAGGATT TGTTGCCTTT TCATTGATTA 25 GAGACAATAA ATATCTTGTA ACTTCCTAAC CAGATCTGAG CTGTGCTCAC 2401 AATAATAATA ATGAAATCAG ATTCTTTGAT GCTGGACTCA GGAGGGAAAT 2451 CATTAGCCAA CTGTTGACTT ACTTATAGCT \AGATGTCTAT GTGAGAAAGT 2501 ATAATATA TATATACACA TATATATGAC ATGTAAGAGT CACTTTTATT 2551 2601 TATCTGTCTT TGTTCACTTA TGAAGCCGGT AACTGCAGCA GTATGTTGGT 30 2651 GATGTCATGA TGCACAGAAG TCCCATGTGG AGTGTTTTTC CCACACTGAC 2701 AACTTGGCCT CCTTTCTGTG TGTTCAGTCT GTTGTCTGAA CTAACACTCC CGCGAGCACT ATACTCTTTA TACTCTGATC CCCCTAGTTC ATCTTAAATT 2751

1201

1251 1301

2801

2851

AAACTTCCAC CCTCATGACT GGAATGGAAG AGGGGACCGA GAGCCTCACA

ATCTCGGAGA GGGAGGAGAA ATTCTTAAAA ACAGCTGCTC TCCTGCGCCC

AGCTTCACAG GCAGCCCTGC CCCTTTCTCC TCACCAGCAT GGTACCTGCC

TGTCTGTGGC CCTGGCAAGA TAGCGTACAC AAGATTCCAT GACTCCAGAG

CATCTTGAAG AAACATACAT ATTTTGAAAG AGGGGAAATG TAGCAGATAG

		2901	TTCACAAGCT GCGGGTTGTA GCTAAATATT CCATTTCTTT GAAATCATGT
	5	2951 <b>\</b>	TTCTAAATTC TTTACCATCA GAAAGAAAAG GAGTGTCATA CACTTTCAAG
		3001	GGAAGGCTTG GTCTGCGTTT TCTGTGTTTG GATTATTTTT ATACTTTGCT
		3051	GATCTTTAAG CTATCCATGG GGGAAATTTT ATACCAACGA GTTAATAATT
		3101	CTCATTCATC GTTTACACAA TGTAACATGT GTCATACTGG GGCCAGCGAG
		3151	ATGGCTCAGT AGGTAAAGGT GCTTGATGCT AAGCCCGGCA GCCTGTGTTT
		3201	CATCTAÇAGG ATGCACAACA TAAAAGAAAA GATCTGATTC CCACAGGTTC
		3251	TCTTCTGACC TACACACA CACACTAAAA TAACATTTAA AAATATGTGC
		3301	CAAATTATA TTGTTCGGGT GCCACCTTCC ACCAGCTTAC CACTACGGTA
	10	3351	GAACTGTCAA ATTCATCTCC CTGAATTTGT CTTAAAGGGG TGTCCATGCA
		3401	CAGGCCCAAG ACTCACCTCC AATGAAATAA ATGTAATACT GAAGTATGCC
	15	3451	ATGATGTTTG TTGTTTCTT TCATCGTAAG CCTGTAAGCA GGAAAAATAC
		3501	GTCAAATCAG ATAGAATAGA GCATTTACCA GTGGTCGATG GCCTGGTCAG
		3551	TCCTGTGCCG GGTGACTTAG GACCAGGCAC GTCAGCTCTC TGAGCCTCCC
The state of the s		3601	CTTCCCTTGT TGTCACAAGG GAATAGAAGC AGAAGAAGCT GAGAGCCTCC
		3651	CTATTCCCAG ATGCCCTGGT GGAATGACCT GCCTCTCTGC CGTTTCTGCC
		3701	AACGTGTTGG TGCTATAAGC TGCTTCAAAT ACCAGTTTGT CTGTAGTGTG
		3751	TACTCACCTA ATCACTTGTT ATCCAGTGCC TGTTCTAGGT TTATGGACTT
Bud find find fine	20	3801	AACTATTTCT GTGATGTTTC ATTTTTAGCC ATGTTAACTC CTAACACATA
		3851	TTCTCTTATG TCTCAGTAAA GTTTCATTTG ATAAGTTGTT GAGATTCTGT
		3901	TATTTGATAA TATTCTTCGG CTGTCCATCC AGCATCTTAA TCACTTTAAA
		3951	ACTGTGATTG TTATTTGCAA CTCTGTTCTT TGGAAAGAAT AAAAGCATTT
		4001	TTTTTCACTT GCTAACATGC TCACAAATGT GAGAGAAGAG TCATTAAAAG
	/	4051	CTTTACTTAC TGGGTCAGTG CGTCATTGAC TCCTTTCTGT GTTTTGCCCA
W.	25	4101	ATAAATTAAT AAAAGACCAA AAAAAAAAAA AAAAAAAA AAAAAAA
/			The state of the s

## **SEQ ID NO:3:** cDNA sequence of mGγ12, variant 2

30	1	CCACCCCCCC	000000000	~~~~		
50	1	GCAGCGGCGG	G CGGCGGCGAC	GACGGCGAAG	AGTTCATATG	GGAAGGACTT
	51	TGGGGTGAGC	ATCTTCTCTA	TTTCCAGCTG	GCTTTTCTGA	TTCACCCCAC
	101	CATTTAAAAC	CTGGAGGCAC	TGGGCCACAC	AAAGCCTTGC	TGATTTTCAG
	151	AAAGAAGACT	CATCAAAGAT	GTCCAGCAAG	ACGGCAAGCA	<b>♥</b> CAACAGCAT
	201	AGCCCAAGCC	AGGAGAACTG	TGCAGCAGCT	GAGATTGGAA	GCTCCATCG

			_	
		251	AAAGAATAAA GGTCTCAAAA GCATCAGCAG ACCTGATGTC ATACTGTGA	G
		301	GAGCATGCCC GGAGCGACCC CCTGCTGATG GGCATACCGA CCTCAGAAA	A
		351	CCCGTTCAAG GATAAGAAGA CCTGCATCAT CTTATAGTGG ACCAGGAAGG	С
		401	CCCCTTGCC TCTTAACGCA AACCACAGCA GCAACCTGAA GGGATTCCT	Т
	5	451	CAGCTTACCT GGTAACCACA GCTAGTAACT AAAACACCCT TCTCTCGGAA	A
		501	TAAYAGACCC TGAAGTCTCT CTTTTTCAAG TTGTCCTTTC TTCACCCTT	Г
		551	ACTGATTAA TACAGAATAA CAATCTTATT TTCTATTTGA TAACTATGG	Г
		601	ATCATA TGG GTTACTGTAT AAGGAAAATG GCAGGGGAGT TGTGGGAAGG	2
		651	TTGTCTTTAC AAAATATAAT TGATTAAGAT ATGTCAAGAC CTACATTGTC	7
	10	701	TAAGCACCG CAAATTAAAA TGTCGAGAAT CACTTCAGTC AAAAACCTTT	Г
		751	ATATTCTGTT\CTTAATAATG TTTGTGCCAA CCTATATCCC ATGTAAGGGA	Į.
192. 3 - 192. 193 193. 193 193.		801	TCTGGGGAGG AGGCATGTGT CTACAACCAT ACCTTTTTGC ACTATGGGCA	Ŧ.
ij		851	CTAACCACCC TGAAACTTCC TGCGGTAGCT CCCTCCCTTC AGAGTTACAT	[
The state of the s		901	CATTATCCTG ACTCTGTGTA GGTAAATTTC CGTGAAATTT TTGTACAAAA	7
2 22	15	951	AAAAGGTAAT GAAAGACGT TGCAAAGATC ATCTGCATTA TAATGAGTTG	<b>1</b>
	20	1001	ATGCTGTTCT CACTCCTCTC TTGGAATTGT GCTGGCCCCT TAGTCTACAA	L
t No.		1051	TAAACTGTGC CAATTAAAAA CCTAAGGCTA AAACTGAAAG CCCTTTGATG	;
		1101	GGGTCTTAAC TCATATCAGT CATTTGGGCT TCTCTGATCC TGAGGCTAAG	ŕ
		1151	AAAGGGGAAG AGACCCTCAG GAGGCAGCTT CCACTCCAGG GCTCTTGATC	
other Property and Communication of the Communicati		1201	TCTGCTGGAT TGGGGGTGGC CACCTCAGAA ACTTCCACCC TCATGACTGG	÷
įį		1251	AATGGAAGAG GGGACCGAGA CCCTCACAAT CTCGGAGAGG GAGGAGAAAT	
0.5		1301	TCTTAAAAAC AGCTGCTCTC CTGCCCAG CTTCACAGGC AGCCCTGCCC	
pur		1351	CTTTCTCCTC ACCAGCATGG TACTGCCCT TACTGCTAGA GCAGCTGCTT	
10 X		1401	GTAGAGGGAC ATTCCCTCCT TCCCAGTTTT AACTGGTGGA CCACAGTGGG	
W.	25	1451	GGGAAAAACA TTCAAGCGAT ATAAAGACAC TTGGGCTCTT TGCAGATGCC	
		1501	TATACTTCCA ACACTACCAT GTCCACAAAC CACCCTGGGG GAGGGCCCTT	
		1551	CCAAAGGGAG GCTTGCTAGT TTCAGCGTCT AGCAGTTGGG TCCTCACTTT	
		1601	TACTCCAATT GTGAAAATAG CCCACGTAGC CTCGCAGTGT CCAGTAGGGA	
		1651	TCCCAGAGGC ACATAACCAA GAAAGGATTT TGACTTTGTC ACAGTGACTA	
	30	1701	TTTAAAATAA TCTATTCGAA GTCCAAACCA AACACAAAGC CTGTGATATT	
		1751	TTAGGTTATT AAGGTAACTG CTAATGAAGG ATTTTAAAAA GTGTCCTCAA	
			AAAGGACTTA GCCCCGGGAG TTGTTTATAA AATTTCCCCC ACTTGTATAC	
			AGTGTGCACT AAAAGAAAAT GTATTTTAAT ATCTAATGCC TGGGCTCTGA	
		1901	GCGTCATGCT TCTTGGTGGT AAACATGCAG TCCTGTTCCT AAGTGACTCA	

dente ant dente dans south it at, those in	

	1954	GAGGCATCAG AATTTCTCCA CGTTACCCAT CTGCTTGGCA CTCGGAACTG	3
	2001	igg angle AGCGTGTGAA ATCCATAGCG CTGCCCACAA CCTGTTCTCA CTGCTTAGCT	-
	2051	CCCAGCTGGA TTAAAGACAC CTGCTCAGGC GGGAGAGAGA GAGAGAGAGA	7
	2101	AGCTTTTAC CTTGGAAAAG GTAAAGATGG AAATGTACAC CAAAAAAGAC	1
5	2151	AATTTTTACA TTTAATGGAA CATTCTTTTT TTTTACAAGT ATATTTTTCT	,
	2201	ACTOATAGTT TCAGAACACT AATCTTATAT TCACTCTAAT CTTAAACATG	;
	2251	TTTCTTAAA TATTTATAAG GCAGTTTATT ACAGAATATT TTCATGCAAT	
	2301	CATGTG CACA TTATTGGTAG CAAACATAGT ATATCCTTTA GTACTTTAGC	
	2351	ATATTTTTGT TAAAATACTT TTAATGGTAA GAAATGAACT TGAGGTCCCA	
10	2401	GGAGGTTTTG TTGCCTTTTC ATTGATTAGA GACAATAAAT ATCTTGTAAC	
	2451	TTCCTAACCA GATCTGAGCT GTGCTCACAA TAATAATAAT GAAATCAGAT	
	2501	TCTTTGATGC TGGACTCAGG AGGGAAATCA TTAGCCAACT GTTGACTTAC	
	2551	TTATAGCTAG ATGTCTATGT GAGAAAGTAT AATATATATA TATACACATA	
	2601	TATATGACAT GTAAGAGTCA CTTTTATTTA TCTGTCTTTG TTCACTTATG	
15	2651	AAGCCGGTAA CTGCAGCAGT ATGTTGGTGA TGTCATGATG CACAGAAGTC	
	2701	CCATGTGGAG TGTTTTTCCC ACACTGACAA CTTGGCCTCC TTTCTGTGTG	
	2751	TTCAGTCTGT TGTCTGAACT AACACTCCCG CGAGCACTAT ACTCTTTATA	
	2801	CTCTGATCCC CCTAGTTCAT CTTAAATTTG TCTGTGGCCC TGGCAAGATA	
	2851	GCGTACACAA GATTCCATGA CTCCAGAGCA TCTTGAAGAA ACATACATAT	
20	2901	TTTGAAAGAG GGGAAATGTA CAGAAGCTGC GGGTTGTAGC	
	2951	TAAATATTCC ATTTCTTTGA AATCATGTTT CTAAATTCTT TACCATCAGA	
	3001	AAGAAAAGGA GTGTCATACA CTTTCAAGGG AAGGCTTGGT CTGCGTTTTC	
	3051	TGTGTTTGGA TTATTTTTAT ACTTTGCTGA TCTTTAAGCT ATCCATGGGG	
) <del>,</del>	3101	GAAATTTTAT ACCAACGAGT TAATAATTCT CATTCATCGT TTACACAATG	
25	3151	TAACATGTGT CATACTGGGG CCAGCGAGAT GGCTCAGTAG GTAAAGGTGC	
	3201	TTGATGCTAA GCCCGGCAGC CTGTGTT CA TCTACAGGAT GCACAACATA	
	3251	AAAGAAAAGA TCTGATTCCC ACAGGTTCCC TTCTGACCTA CACACACA	
	3301	CACTAAAATA ACATTTAAAA ATATGTGCCA AATTATATTT GTTCGGGTGC	
	3351	CACCTTCCAC CAGCTTACCA CTACGGTAGA CTGTCAAAT TCATCTCCCT	
30	3401	GAATTTGTCT TAAAGGGGTG TCCATGCACA GCCCCAAGAG TCACCTCCAA	
	3451	TGAAATAAAT GTAATACTGA AGTATGCCAT GATGTTTGTT GTTTTCTTTC	
	3501	ATCGTAAGCC TGTAAGCAGG AAAAATACGT CAAATCAGAT AGAATAGAGC	
	3551	ATTTACCAGT GGTCGATGGC CTGGTCAGTC CTGTGCGGG TGACTTAGGA	
	3601	CCAGGCACGT CAGCTCTCTG AGCCTCCCCT TCCCTTGTTG TCACAAGGGA	

	3651	ATAGAAGCAG	AAGAAGCTGA	GAGCCTCCCT	ATTCCCAGAT	GCCCTGGTGG
	3701	AATGACCTGC	CTCTCTGCCG	TTTCTGCCAA	CGTGTTGGTG	CTATAAGCTG
5	3751	TTCAAATAC	CAGTTTGTCT	GTAGTGTGTA	CTCACCTAAT	CACTTGTTAT
	3801	CONGTECCTE	TTCTAGGTTT	ATGGACTTAA	CTATTTCTGT	GATGTTTCAT
	3851	TTTTAGCCAT	GTTAACTCCT	AACACATATT	CTCTTATGTC	TCAGTAAAGT
	3901	TTCATTTGAT	AAGTTGTTGA	GATTCTGTTA	TTTGATAATA	TTCTTCGGCT
	3951	GTCCATCCAG	CATCTTAATC	ACTTTAAAAC	TGTGATTGTT	ATTTGCAACT
	4001	CTGTTCTTTG	GAAAGAATAA	AAGCATTTTT	TTTCACTTGC	TAACATGCTC
	4051	ACAAATGTGA	GAGAAGAGTC	ATTAAAAGCT	TTACTTACTG	GGTCAGTGCG
	4101	TCATTGACTC	CTTTCTGTGT	TTTGCCCAAT	AAATTAATAA	AAGACCAAAA
	4151	AAAAAAAAA	AAAAAAAA	AAAAA		

15 m

**SEQ ID NO:4** 

amino acid sequence of human Gy12

- 1. MSSKTASTNN IAQARRTVQQ LRLEASIERI KVSKASADLM SYCEEHARSD
- 51. PLLIGIPTSE NPFKDKKTCI IL